



A. Navarro

1645

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/684,883

DATE: 07/30/2002
TIME: 14:21:00

Input Set : N:\Crf3\RULE60\09684883.raw
Output Set: N:\CRF3\07302002\I684883.raw

PT#9

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Brodeur, Bernard R
6 Martin, Denis
7 Hamel, Josee
8 Rioux, Clement

10 (ii) TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
11 OF NEISSERIA MENINGITIDIS

13 (iii) NUMBER OF SEQUENCES: 30

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Foley & Lardner
17 (B) STREET: 3000 K Street, N.W., Suite 500
18 (C) CITY: Washington
19 (D) STATE: D.C.
20 (E) COUNTRY: USA
21 (F) ZIP: 20007-5109

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

ENTERED

RECEIVED

AUG 06 2002

TECH CENTER 1600/2900

C--> 30 (A) APPLICATION NUMBER: US/09/684,883
C--> 31 (B) FILING DATE: 06-Oct-2000

42 (vi) CURRENT APPLICATION DATA:

34 (A) APPLICATION NUMBER: US/08/913,362
35 (B) FILING DATE: 13-NOV-1997
39 (A) APPLICATION NUMBER: US 08/406,362
40 (B) FILING DATE: 17-MAR-1995
43 (A) APPLICATION NUMBER: US 60/001,983
44 (B) FILING DATE: 04-AUG-1995

46 (viii) ATTORNEY/AGENT INFORMATION:

47 (A) NAME: Bent, Stephen A.
48 (B) REGISTRATION NUMBER: 29,768
49 (C) REFERENCE/DOCKET NUMBER: 047998/0128

51 (ix) TELECOMMUNICATION INFORMATION:

52 (A) TELEPHONE: (202)672-5300
53 (B) TELEFAX: (202)672-5399
54 (C) TELEX: 904136

57 (2) INFORMATION FOR SEQ ID NO: 1:

59 (i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 830 base pairs
61 (B) TYPE: nucleic acid

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62      (C) STRANDEDNESS: double
63      (D) TOPOLOGY: linear
65      (ii) MOLECULE TYPE: DNA (genomic)
67      (iii) HYPOTHETICAL: NO
69      (iv) ANTI-SENSE: NO
71      (vi) ORIGINAL SOURCE:
72          (A) ORGANISM: Neisseria meningitidis
73          (B) STRAIN: 608B
75      (ix) FEATURE:
76          (A) NAME/KEY: CDS
77          (B) LOCATION: 143..667
79      (ix) FEATURE:
80          (A) NAME/KEY: sig_peptide
81          (B) LOCATION: 143..199
83      (ix) FEATURE:
84          (A) NAME/KEY: mat_peptide
85          (B) LOCATION: 200..667
88      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
90 TCGGCAAAGC AGCCGGATAC CGCTACGTAT CTTGAAGTAT TGAAAATATT ACGATGCAAA 60
92 AAAGAAAATT TAAGTATAAT ACAGCAGGAT TCTTTAACGG ATTCTTAACA ATTTTCTAA 120
94 CTGACCATAA AGGAACCAAA AT ATG AAA AAA GCA CTT GCC ACA CTG ATT GCC 172
95           Met Lys Lys Ala Leu Ala Thr Leu Ile Ala
96           -19          -15          -10
98 CTC GCT CTC CCG GCC GCA CTG GCG GAA GGC GCA TCC GGC TTT TAC 220
99 Leu Ala Leu Pro Ala Ala Ala Leu Ala Glu Gly Ala Ser Gly Tyr
100           -5           1           5
102 GTC CAA GCC GAT GCC GCA CAC GCA AAA GCC TCA AGC TCT TTA GGT TCT 268
103 Val Gln Ala Asp Ala Ala His Ala Lys Ala Ser Ser Ser Leu Gly Ser
104           10          15          20
106 GCC AAA GGC TTC AGC CCG CGC ATC TCC GCA GGC TAC CGC ATC AAC GAC 316
107 Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp
108           25          30          35
110 CTC CGC TTC GCC GTC GAT TAC ACG CGC TAC AAA AAC TAT AAA GCC CCA 364
111 Leu Arg Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro
112           40          45          50          55
114 TCC ACC GAT TTC AAA CTT TAC AGC ATC GGC GCG TCC GCC ATT TAC GAC 412
115 Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp
116           60          65          70
118 TTC GAC ACC CAA TCG CCC GTC AAA CCG TAT CTC GGC GCG CGC TTG AGC 460
119 Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser
120           75          80          85
122 CTC AAC CGC GCC TCC GTC GAC TTG GGC GGC AGC GAC AGC TTC AGC CAA 508
123 Leu Asn Arg Ala Ser Val Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln
124           90          95          100
126 ACC TCC ATC GGC CTC GGC GTA TTG ACG GGC GTA AGC TAT GCC GTT ACC 556
127 Thr Ser Ile Gly Leu Gly Val Leu Thr Gly Val Ser Tyr Ala Val Thr
128           105         110         115
130 CCG AAT GTC GAT TTG GAT GCC GGC TAC CGC TAC AAC TAC ATC GGC AAA 604
131 Pro Asn Val Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys

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132 120 125 130 135 136 140 145 150 134 GTC AAC ACT GTC AAA AAC GTC CGT TCC GGC GAA CTG TCC GTC GGC GTG
 135 Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu Leu Ser Val Gly Val 136 140 145 150 136 Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu Leu Ser Val Gly Val
 138 CGC GTC AAA TTC TGATATGCGC CTTATTCTGC AAACCGCCGA GCCTTCGGCG 139 Arg Val Lys Phe 140 155 138 CGC GTC AAA TTC TGATATGCGC CTTATTCTGC AAACCGCCGA GCCTTCGGCG 139 Arg Val Lys Phe 140 155 142 GTTTGTTT CTGCCACCGC AACTACACAA GCCGGCGTT TTGTACGATA ATCCCGAATG 143 CTGCGGCTTC TGCCGCCCTA TTTTGAGG AATCCGAAAT GTCCAAAACC ATCATCCACA 144 CTGCGGCTTC TGCCGCCCTA TTTTGAGG AATCCGAAAT GTCCAAAACC ATCATCCACA 145 CCGACA 146 CCGACA
 149 (2) INFORMATION FOR SEQ ID NO: 2:
 151 (i) SEQUENCE CHARACTERISTICS:
 152 (A) LENGTH: 174 amino acids
 153 (B) TYPE: amino acid
 154 (D) TOPOLOGY: linear
 156 (ii) MOLECULE TYPE: protein
 158 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 160 Met Lys Ala Leu Ala Thr Leu Ile Ala Leu Ala Leu Pro Ala Ala
 161 -19 -15 -10 -5
 163 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala
 164 1 5 10
 166 His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro
 167 15 20 25
 169 Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp
 170 30 35 40 45
 172 Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu
 173 50 55 60
 175 Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro
 176 65 70 75
 178 Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val
 179 80 85 90
 181 Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln Thr Ser Ile Gly Leu Gly
 182 95 100 105
 184 Val Leu Thr Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp
 185 110 115 120 125
 187 Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn
 188 130 135 140
 190 Val Arg Ser Gly Glu Leu Ser Val Gly Val Arg Val Lys Phe
 191 145 150 155
 194 (2) INFORMATION FOR SEQ ID NO: 3:
 196 (i) SEQUENCE CHARACTERISTICS:
 197 (A) LENGTH: 710 base pairs
 198 (B) TYPE: nucleic acid
 199 (C) STRANDEDNESS: double
 200 (D) TOPOLOGY: linear
 202 (ii) MOLECULE TYPE: DNA (genomic)
 204 (iii) HYPOTHETICAL: NO
 206 (iv) ANTI-SENSE: NO
 208 (vi) ORIGINAL SOURCE:

RAW SEQUENCE LISTING
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209      (A) ORGANISM: Neisseria meningitidis
210      (B) STRAIN: MCH88
212      (ix) FEATURE:
213          (A) NAME/KEY: CDS
214          (B) LOCATION: 116..643
216      (ix) FEATURE:
217          (A) NAME/KEY: sig_peptide
218          (B) LOCATION: 116..172
220      (ix) FEATURE:
221          (A) NAME/KEY: mat_peptide
222          (B) LOCATION: 173..643
225      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
227 GTATCTTGAG GCATTGAAAA TATTACAATG CAAAAAGAAA ATTCAGTAT AATACGGCAG 60
229 GATTCTTAA CGGATTCTTA ACCATTTTC TCCCTGACCA TAAAGGAATC AAGAT ATG 118
230                                         Met
231                                         -19
233 AAA AAA GCA CTT GCC GCA CTG ATT GCC CTC CCG GCC GCC GCA 166
234 Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala Ala
235     -15           -10           -5
237 CTG GCG GAA GGC GCA TCC GGC TTT TAC GTC CAA GCC GAT GCC GCA CAC 214
238 Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala His
239     1           5           10
241 GCC AAA GCC TCA AGC TCT TTA GGT TCT GCC AAA GGC TTC AGC CCG CGC 262
242 Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro Arg
243     15          20          25          30
245 ATC TCC GCA GGC TAC CGC ATC AAC GAC CTC CGC TTC GCC GTC GAT TAC 310
246 Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp Tyr
247     35          40          45
249 ACG CGC TAC AAA AAC TAT AAA CAA GTC CCA TCC ACC GAT TTC AAA CTT 358
250 Thr Arg Tyr Lys Asn Tyr Lys Gln Val Pro Ser Thr Asp Phe Lys Leu
251     50          55          60
253 TAC AGC ATC GGC GCG TCC GCC ATT TAC GAC TTC GAC ACC CAA TCC CCC 406
254 Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro
255     65          70          75
257 GTC AAA CCG TAT CTC GGC GCG CGC TTG AGC CTC AAC CGC GCC TCC GTC 454
258 Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val
259     80          85          90
261 GAC TTT AAC GGC AGC GAC AGC TTC AGC CAA ACC TCC ACC GGC CTC GGC 502
262 Asp Phe Asn Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu Gly
263     95          100         105         110
265 GTA TTG GCG GGC GTA AGC TAT GCC GTT ACC CCG AAT GTC GAT TTG GAT 550
266 Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp
267     115         120         125
269 GCC GGC TAC CGC TAC AAC TAC ATC GGC AAA GTC AAC ACT GTC AAA AAT 598
270 Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn
271     130         135         140
273 GTC CGT TCC GGC GAA CTG TCC GCC GGC GTA CGC GTC AAA TTC TGATATAACGC 650
274 Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe
275     145         150         155

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277 GTTATTCCGC AAACGCCGA GCCTTCGGC GGTTTGTT TCCGCCGCCG CAACTACACA 710

281 (2) INFORMATION FOR SEQ ID NO: 4:

283 (i) SEQUENCE CHARACTERISTICS:

284 (A) LENGTH: 175 amino acids

285 (B) TYPE: amino acid

286 (D) TOPOLOGY: linear

288 (ii) MOLECULE TYPE: protein

290 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

292 Met Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala

293 -19 -15 -10 -5

295 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala

296 1 5 10

298 His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro

299 15 20 25

301 Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp

302 30 35 40 45

304 Tyr Thr Arg Tyr Lys Asn Tyr Lys Gln Val Pro Ser Thr Asp Phe Lys

305 50 55 60

307 Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser

308 65 70 75

310 Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser

311 80 85 90

313 Val Asp Phe Asn Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu

314 95 100 105

316 Gly Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu

317 110 115 120 125

319 Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys

320 130 135 140

322 Asn Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe

323 145 150 155

326 (2) INFORMATION FOR SEQ ID NO: 5:

328 (i) SEQUENCE CHARACTERISTICS:

329 (A) LENGTH: 850 base pairs

330 (B) TYPE: nucleic acid

331 (C) STRANDEDNESS: double

332 (D) TOPOLOGY: linear

334 (ii) MOLECULE TYPE: DNA (genomic)

336 (iii) HYPOTHETICAL: NO

338 (iv) ANTI-SENSE: NO

340 (vi) ORIGINAL SOURCE:

341 (A) ORGANISM: Neisseria meningitidis

342 (B) STRAIN: Z4063

344 (ix) FEATURE:

345 (A) NAME/KEY: CDS

346 (B) LOCATION: 208..732

348 (ix) FEATURE:

349 (A) NAME/KEY: sig_peptide

350 (B) LOCATION: 208..264

352 (ix) FEATURE:

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/30/2002
PATENT APPLICATION: US/09/684,883 TIME: 14:21:01

Input Set : N:\Crf3\RULE60\09684883.raw
Output Set: N:\CRF3\07302002\I684883.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:30; Xaa Pos.7,73,126

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/684,883

DATE: 07/30/2002
TIME: 14:21:01

Input Set : N:\Crf3\RULE60\09684883.raw
Output Set: N:\CRF3\07302002\I684883.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:1050 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:1062 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:64
L:1071 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:112